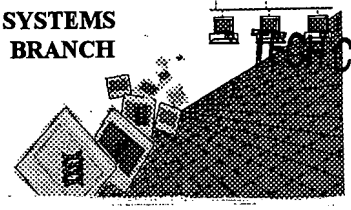
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/267,963B
Source: 1600
Date Processed by STIC: 3/27/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Errors begin on p. 2

RAW SEQUENCE LISTING DATE: 03/27/2003
PATENT APPLICATION: **US/09/267,963B** TIME: 10:28:32

Input Set : **A:\lud 5539.1 sequence listing March 2001.ascii.txt**
Output Set: **N:\CRF4\03272003\I267963B.raw**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE

(ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING IT, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.L.P.

(B) STREET: 666 Fifth Avenue

(C) CITY: New York City

(D) STATE: New York

(E) COUNTRY: USA

(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: PC-DOS

(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

C--> **(A) APPLICATION NUMBER: US/09/267,963B**

C--> **(B) FILING DATE: 08-Mar-2001**

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/GB93/02367

(B) FILING DATE: November 17, 1993

(A) APPLICATION NUMBER: GB 9224057.1

(B) FILING DATE: November 17, 1992

(A) APPLICATION NUMBER: GB 9304677.9

(B) FILING DATE: March 8, 1993

(A) APPLICATION NUMBER: GB 9304680.3

(B) FILING DATE: March 8, 1993

(A) APPLICATION NUMBER: 9311047.6

(B) FILING DATE: May 28, 1993

(A) APPLICATION NUMBER: 9313763.6

(B) FILING DATE: July 2, 1993

(A) APPLICATION NUMBER: 9136099.2

(B) FILING DATE: August 3, 1993

(A) APPLICATION NUMBER: 321344.5

(B) FILING DATE: October 15, 1993

(A) APPLICATION NUMBER: 09/039,177

(B) FILING DATE: March 13, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mary Anne Schofield

RAW SEQUENCE LISTING DATE: 03/27/2003
PATENT APPLICATION: US/09/267,963B TIME: 10:28:32

Input Set : A:\lud 5539.1 sequence listing March 2001.ascii.txt
Output Set: N:\CRF4\03272003\I267963B.raw

```
69          (B) REGISTRATION NUMBER: 36,669
70          (C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS
72     (ix) TELECOMMUNICATION INFORMATION:
73          (A) TELEPHONE: (212) 318-3000
74          (B) TELEFAX: (212) 318-3400
```

ERRORED SEQUENCES

```
2665 (2) INFORMATION FOR SEQ ID NO: 32:
2666      (i) SEQUENCE CHARACTERISTICS:
2667           (A) LENGTH: 175 amino acids
2668           (B) TYPE: amino acid
2669           (D) TOPOLOGY: linear
2671      (ii) MOLECULE TYPE: peptide
2673      (vi) ORIGINAL SOURCE:
2674           (A) ORGANISM: Mouse
2676      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
2678 Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
2679                 5                  10                  15
2680 Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp
2681             20                  25                  30
2682 Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met
2683         35                  40                  45
2684 Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr
2685     50                  55                  60
2686 Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly
2687 65                  70                  75                  80
2688 Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu
2689                 85                  90                  95
2690 Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu
2691             100                 105                 110
2692 Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg
2693         115                 120                 125
2694 Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys
2695     130                 135                 140
2696 Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala
2697 145                 150                 155                 160
2698 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
E--> 2699
                                                    165                 170
2821 (2) INFORMATION FOR SEQ ID NO: 35:
2822      (i) SEQUENCE CHARACTERISTICS:
2823           (A) LENGTH: 536 amino acids
2824           (B) TYPE: amino acid
2825           (D) TOPOLOGY: linear
2827      (ii) MOLECULE TYPE: peptide
2829      (vi) ORIGINAL SOURCE:
2830           (A) ORGANISM: MOUSE
2832      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Misaligned amino numbering throughout.

See error summary sheet item 3

```
2834 Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
2835                 5                  10                  15
2836 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
2837             20                  25                  30
2838 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
2839         35                  40                  45
2840 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
2841     50                  55                  60
2842 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
2843 65                  70                  75                  80
2844 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
2845                 85                  90                  95
2846 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
2847             100                 105                 110
2848 Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
2849         115                 120                 125
2850 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
2851     130                 135                 140
2852 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
2853 145                 150                 155                 160
2854 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
2855                 165                 170                 175
2856 Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
2857             180                 185                 190
2858 Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu
2859         195                 200                 205
2860 Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
2861     210                 215                 220
2862 Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val
2863 225                 230                 235                 240
2864 Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu
2865                 245                 250                 255
2866 Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile
2867             260                 265                 270
2868 Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile
2869         275                 280                 285
2870 Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn
2871     290                 295                 300
2872 Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg
2873 305                 310                 315                 320
2874 Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly
2875                 325                 330                 335
2876 His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu
2877             340                 345                 350
2878 Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val
2879         355                 360                 365
2880 Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly
2881     370                 375                 380
2882 Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe
```

RAW SEQUENCE LISTING DATE: 03/27/2003
PATENT APPLICATION: **US/09/267,963B** TIME: 10:28:32

Input Set : **A:\lud 5539.1 sequence listing March 2001.ascii.txt**
Output Set: **N:\CRF4\03272003\I267963B.raw**

```
     385                 390                 395                 400
     Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val
                    405                 410                 415
     Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp
                420                 425                 430
     Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu
            435                 440                 445
     Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile
        450                 455                 460
     Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr
     465                 470                 475                 480
     Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly
                    485                 490                 495
     Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr
                500                 505                 510
     Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp
E--> 2899
                                                    515                 520                 525
     Leu Leu Pro Lys Glu Ser Ser Ile
E--> 2901                       530                 535
     (2) INFORMATION FOR SEQ ID NO: 37:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 102 amino acids
                         (B) TY7PE: amino acid
               (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: peptide
          (vi) ORIGINAL SOURCE:
               (A) ORGANISM: C. elegans
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
     Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala Arg Thr Thr Gly Trp
E--> 3005
                                                            5                   10
     Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp Arg Ser Phe Tyr Glu
E--> 3007                                       20                  25                  30
     Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln Ser Ala Arg Pro Ser
E--> 3009
                                                        35                  40                  45
     Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu Lys Ser Val Thr Asp
E--> 3011                                           50                  55                  60
     Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val Cys Thr Asn Asn Thr
E--> 3013
                                                        65                  70                  75
     Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys Asp Lys Gly Asn Phe
E--> 3015
                                                                85                  90                  100
E--> 3016 Cys
     (2) INFORMATION FOR SEQ ID NO: 38:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 6 amino acids
               (B) TYPE: amino acid
               (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: peptide
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
```

3032 Asp Leu Lys Pro Glu Asn

RAW SEQUENCE LISTING DATE: 03/27/2003
PATENT APPLICATION: **US/09/267,963B** TIME: 10:28:32

Input Set : **A:\lud 5539.1 sequence listing March 2001.ascii.txt**
Output Set: **N:\CRF4\03272003\I267963B.raw**

E--> 3033 5
3038 (2) INFORMATION FOR SEQ ID NO: 39:
3039 (i) SEQUENCE CHARACTERISTICS:
3040 (A) LENGTH: 6 amino acids
3041 (B) TYPE: amino acid
3042 (D) TOPOLOGY: linear
3044 (ii) MOLECULE TYPE: peptide
3046 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
3048 Asp Leu Ala Ala Arg Asn
E--> 3049 5
3051 (2) INFORMATION FOR SEQ ID NO: 40:
3052 (i) SEQUENCE CHARACTERISTICS:
3053 (A) LENGTH: 6 amino acids
3054 (B) TYPE: amino acid
3055 (D) TOPOLOGY: linear
3057 (ii) MOLECULE TYPE: peptide
3059 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
3061 Asp Ile Lys Ser Lys Asn
E--> 3062 5
3065 (2) INFORMATION FOR SEQ ID NO: 41:
3066 (i) SEQUENCE CHARACTERISTICS:
3067 (A) LENGTH: 6 amino acids
3068 (B) TYPE: amino acid
3069 (D) TOPOLOGY: linear
3071 (ii) MOLECULE TYPE: peptide
3073 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
3075 Asp Phe Lys Ser Lys Asn
E--> 3076 5
3079 (2) INFORMATION FOR SEQ ID NO: 42:
3080 (i) SEQUENCE CHARACTERISTICS:
3081 (A) LENGTH: 6 amino acids
3082 (B) TYPE: amino acid
3083 (D) TOPOLOGY: linear
3085 (ii) MOLECULE TYPE: peptide
3087 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
3089 Asp Leu Lys Ser Ser Asn
E--> 3090 5
3093 (2) INFORMATION FOR SEQ ID NO: 43:
3094 (i) SEQUENCE CHARACTERISTICS:
3095 (A) LENGTH: 6 amino acids
3096 (B) TYPE: amino acid
3097 (D) TOPOLOGY: linear
3099 (ii) MOLECULE TYPE: peptide
3101 (ix) FEATURE:
3102 (D) OTHER INFORMATION: First Xaa is Thr or Ser;
3103 fourth Xaa is Tyr or Phe;Each other Xaa
3104 may be any amino acid
3106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
W--> 3108 Gly Xaa Xaa Xaa Xaa Xaa

RAW SEQUENCE LISTING DATE: 03/27/2003
PATENT APPLICATION: US/09/267,963B TIME: 10:28:32

Input Set : A:\lud 5539.1 sequence listing March 2001.ascii.txt
Output Set: N:\CRF4\03272003\I267963B.raw

E--> 3109 5
3112 (2) INFORMATION FOR SEQ ID NO: 44:
3113 (i) SEQUENCE CHARACTERISTICS:
3114 (A) LENGTH: 6 amino acids
3115 (B) TYPE: amino acid
3116 (D) TOPOLOGY: linear
3118 (ii) MOLECULE TYPE: peptide
3120 (ix) FEATURE:
3121 (D) OTHER INFORMATION: Fisrt Xaa is any amino acid;
3122 second Xaa is Ile or Val;
3123 third Xaa is Lys or Arg;
3124 fourth Xaa is Thr or Met.
3126 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
W--> 3128 **Xaa Pro Xaa Xaa Trp Xaa**
E--> 3129 5
3132 (2) INFORMATION FOR SEQ ID NO: 45:
3133 (i) SEQUENCE CHARACTERISTICS:
3134 (A) LENGTH: 6 amino acids
3135 (B) TYPE: amino acid
3136 (D) TOPOLOGY: linear
3138 (ii) MOLECULE TYPE: peptide
3140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
3142 Gly Thr Arg Arg Tyr Met
E--> 3143 5
3145 (2) INFORMATION FOR SEQ ID NO: 46:
3146 (i) SEQUENCE CHARACTERISTICS:
3147 (A) LENGTH: amino acids
3148 (B) TYPE: amino acid
3149 (D) TOPOLOGY: linear
3151 (ii) MOLECULE TYPE: peptide
3153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3155 Gly Thr Ala Arg Tyr Met
E--> 3156 5

VERIFICATION SUMMARY DATE: 03/27/2003
PATENT APPLICATION: **US/09/267,963B** TIME: 10:28:33

Input Set : **A:\lud 5539.1 sequence listing March 2001.ascii.txt**
Output Set: **N:\CRF4\03272003\I267963B.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:88 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:335 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:608 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1153 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1409 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1655 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1915 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2170 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2416 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2434 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2470 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2488 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2506 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2524 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:2699 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:0 M:200 E: Mandatory Header Field missing, Seq 34, [(B) TYPE:] of (2)(i)
L:2899 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
M:332 Repeated in SeqNo=35
L:0 M:200 E: Mandatory Header Field missing, Seq 37, [(B) TYPE:] of (2)(i)
L:3005 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
M:332 Repeated in SeqNo=37
L:3016 M:203 E: No. of Seq. differs, LENGTH:Input:102 Found:97 SEQ:37
L:3033 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:3049 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:3062 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:3076 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:3090 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:3108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
M:332 Repeated in SeqNo=43
L:3128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
M:332 Repeated in SeqNo=44
L:3143 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:3156 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
L:3156 M:203 E: No. of Seq. differs, LENGTH:Input:0 Found:6 SEQ:46

AU Hopkins W E; Westerhausen D R; Fujii S; Billadello J J; Sobel B E
TI Mediators of induction of augmented expression of plasminogen activator inhibitor type-1 in Hep G2 cells by platelets.
SO THROMBOSIS AND HAEMOSTASIS, (1991 Aug 1) 66 (2) 239-45.
Journal code: VQ7. ISSN: 0340-6245.
AN 92124428 MEDLINE
JT THROMBOSIS AND HAEMOSTASIS
JT Thromb Haemost
LA English
AB Plasminogen activator inhibitor type-1 (PAI-1) is a physiologic modulator of the fibrinolytic system. We have shown previously that PAI-1 biosynthesis in cultured cells depends on several factors in serum. Because platelets are richly endowed with specific growth factors and because the release reaction is an integral part of thrombosis, the present study was performed to determine whether platelets augment PAI-1 production and if so, to define mediators responsible. Hep G2 cells were used to determine whether platelet lysates increased PAI-1 synthesis in a dose and time-dependent manner. In cells labeled metabolically with 35S-methionine for 6 h, an increase in labeled PAI-1 was elicited indicative of de novo synthesis as well as increased secretion of PAI-1 mediated by platelet lysates. Steady state levels of both the 3.2 and 2.2 kb forms of PAI-1 mRNA increased after 2 h and peaked in 3-5 h in a dose-dependent fashion as well. Incubation of Hep G2 cells with collagen activated platelets resulted in a similar induction of PAI-1 mRNA. The increase in PAI-1 mRNA occurred with exposure of the cells to platelet lysates for intervals as brief as 15 min and was not inhibited by cycloheximide indicating its independence of new protein synthesis. In order to identify the factors in platelets responsible for the induction of PAI-1 synthesis in the Hep G2 cell model system, neutralizing antibodies were used to inhibit specific platelet associated growth factors. Antibodies to transforming growth factor-beta (TGF-beta) and to the epidermal growth factor (EGF)/transforming growth factor alpha (TGF-alpha) receptor inhibited the platelet lysate-mediated increase in PAI-1 protein by 77%.(ABSTRACT TRUNCATED AT 250 WORDS)

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/267,963B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.